

WHAT IS CLAIMED:

1. An isolated nucleic acid molecule selected from the group consisting of:

5 (i) an isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof which comprises at least 75 nucleotides;

(ii) an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which encodes at least 25 contiguous amino acids of said polypeptide;

10 (iii) an isolated nucleic acid molecule having at least 20-30% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or to a fragment thereof which comprises at least 100 contiguous nucleotides thereof;

15 (iv) an isolated nucleic acid molecule that encodes a polypeptide having at least 40% sequence identity at the amino acid level with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or an isolated nucleic acid molecule encoding at least 50 contiguous amino acid residues thereof;

20 (v) an isolated nucleic acid molecule that encodes a taste receptor or a fragment thereof that specifically hybridizes under stringent hybridization conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23; and

25 (vi) a variant of an isolated nucleic acid molecule according to (i) or (ii), containing at least one substitution, deletion or addition mutation in the coding region.

2. The isolated nucleic acid molecule of Claim 1 which is selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

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3. The isolated nucleic acid molecule of Claim 1 which encodes a polypeptide having an amino acid sequence selected from the group consisting of SEQ

ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof encoding at least 25 contiguous amino acid residues of said polypeptide.

4. An isolated nucleic acid molecule having at least 30% sequence
5 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

5. An isolated nucleic acid molecule having at least 40-60% sequence
10 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

6. An isolated nucleic acid molecule having at least 70% sequence
15 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

7. An isolated nucleic acid molecule having at least 80% sequence
20 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

8. An isolated nucleic acid molecule having at least 90% sequence
25 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

9. An isolated nucleic acid molecule according to Claim 1 which encodes
30 a polypeptide having at least 95% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8,

10, 12, 14, 16, 18, 20, and 24, or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

10. An isolated nucleic acid molecule according to Claim 1 which encodes
5 a polypeptide having at least 96% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

10 11. An isolated nucleic acid molecule according to Claim 1 which encodes a polypeptide having at least 97% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

15 12. An isolated nucleic acid molecule according to Claim 1 which encodes a polypeptide having at least 98% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof that comprises at least 40
20 contiguous amino acids thereof.

13. An isolated nucleic acid molecule according to Claim 1 which encodes a polypeptide having at least 99% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8,
25 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

14. An isolated nucleic acid molecule which exhibits at least 20-30% sequence identity with a nucleic acid sequence selected from the group consisting of
30 SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23 or which exhibits at least 30% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence; and which further contains at least one sequence that encodes a

polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

15. An isolated nucleic acid molecule which exhibits at least 40-60% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or which exhibits at least 40-60% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

16. An isolated nucleic acid molecule that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or at least 70% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof and; which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

17. An isolated nucleic acid molecule that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or at least 90% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

18. An isolated nucleic acid molecule that exhibits at least 85% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or at least 85% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70%

identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

19. An isolated nucleic acid molecule that exhibits at least 90% sequence
5 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or at least 90% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS:
10 25, 26, 27, 28, 29, and 30.

20. An isolated nucleic acid molecule that exhibits at least 95% sequence
identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or at least 95% sequence identity with a
15 fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

21. An isolated nucleic acid molecule that exhibits about 95-99% sequence
20 identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23, or about 95-99% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70%
25 identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

22. An isolated nucleic acid molecule which encodes for a functional taste
receptor that comprises a portion which is at least 100 nucleotides in length that
30 exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23.

23. The nucleic acid molecule of Claim 22 which is a chimeric nucleic acid molecule, wherein said chimeric nucleic acid molecule is produced by combining portions of at least two different G Protein-Coupled Receptors.

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24. The chimeric nucleic acid molecule of Claim 23, wherein said two different G Protein-Coupled Receptors are taste receptors.

25. The chimeric nucleic acid molecule of Claim 23, wherein said chimeric nucleic acid molecule contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said nucleic acid sequences.

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26. An isolated nucleic acid molecule according to Claim 1 which is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

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27. The nucleic acid molecule of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

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28. An isolated nucleic acid molecule which encodes a polypeptide that exhibits about 30-40% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

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29. An isolated nucleic acid molecule which encodes a polypeptide that exhibits about 50% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

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30. An isolated nucleic acid molecule which encodes a polypeptide that exhibits about 60% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

31. An isolated nucleic acid molecule which encodes a polypeptide that exhibits at least 70% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

32. An isolated nucleic acid molecule which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

33. An isolated nucleic acid molecule which encodes a polypeptide that exhibits at least 90% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

34. An isolated nucleic acid molecule which encodes a polypeptide that exhibits at least 95% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment

thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

5 35. An isolated nucleic acid molecule which encodes a polypeptide that exhibits about 95 to 99% sequence identity with a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof comprising at least 40 contiguous amino acids thereof that is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of
10 said polypeptide on the surface of a cell.

 36. An isolated nucleic acid molecule according to Claim 1 which is operably linked to a constitutive promoter.

15 37. An isolated nucleic acid molecule according to Claim 1 which is operably linked to a regulatable promoter.

 38. An isolated nucleic acid molecule according to Claim 1 which is directly or indirectly attached to a nucleic acid sequence encoding a chaperone protein
20 or a fragment thereof.

 39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8,
25 10, 12, 14, 16, 18, 20, and 24.

 40. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 100 amino acids.

30 41. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 150 amino acids.

42. The isolated nucleic acid molecule of Claim 39 wherein the nucleotide sequence encodes at least 200 amino acids.

43. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide sequence encodes at least 250 amino acids.

44. The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is a T2R polypeptide

45. The isolated nucleic acid molecule of Claim 39, wherein the fragment specifically binds a ligand selected from the group consisting of 6-n-propylthiouracil, sucrose octaacetate, raffinose undecaacetate, cycloheximide, denatonium, copper glycinate, and quinine.

46. An isolated nucleic acid molecule according to Claim 1 comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, and 23.

47. An expression vector that comprises a nucleic acid sequence according to Claim 1.

48. The expression vector of Claim 47 which is a mammalian, yeast, bacterial or insect expression vector.

49. A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

50. A cell according to Claim 49, wherein the cell is mammalian.

51. A mammalian cell according to Claim 50, wherein the cell human.

52. A cell according to Claim 49, wherein the cell is yeast or insect.

53. The mammalian cell according to Claim 50 which is selected from the group consisting of a taste cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

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54. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

55. A solid phase which is attached to an array of different nucleic acid sequences which includes at least one sequence according to Claim 1.

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56. The solid phase according to Claim 54 which comprises an array of at least 4 different nucleic acid sequences that encode functional taste receptors or fragments or variants thereof.

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57. A solid phase comprising the nucleic acid array of Claim 54 which comprises at least 10 different nucleic acid sequences that encode functional taste receptors.

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58. A solid phase comprising the nucleic acid array of Claim 54 which comprises at least 50 different nucleic acid sequences that encode taste receptors or fragments or variants thereof.

59. A solid phase comprising the nucleic acid array of Claim 54 which comprises at least 100 different sequences that encode taste receptors or fragments or variants thereof.

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60. An isolated polypeptide or fusion protein that is selected from the group consisting of:

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(i) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24;

(ii) a polypeptide comprising an amino acid sequence that exhibits at least 50% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24;

(iii) a polypeptide comprising an amino acid sequence that exhibits at least 75% sequence identity with a fragment of a polypeptide according to (i) that is at least 40 amino acids in length;

(iv) a chimeric polypeptide that comprises a portion of a polypeptide according to (i) or (ii) that is at least 40 amino acids in length, and a portion of at least one other G Protein-Coupled Receptor; and

(v) a variant of a polypeptide according to (i) which differs by said polypeptide by at least one substitution, addition or deletion modification.

61. An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 60% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

62. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 65% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

63. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 75% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

64. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 75% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

65. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 80% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

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66. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 90% sequence identity with a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24, or a fragment thereof which is at least 200 amino acids.

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67. A variant according to Claim 60(v) which comprises at least 5 conservative amino acid substitutions.

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

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69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

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71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

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72. A solid phase to which is immobilized directly or indirectly at least one isolate polypeptide according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

73. The solid phase of Claim 72 which comprises immobilized at least 4 different polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

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74. The solid phase of Claim 72 which comprises immobilized at least 16 different polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

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75. The solid phase of Claim 72 which comprises immobilized at least 25 different polypeptides according to Claim 48 or a cell which expresses said polypeptide on the surface thereof.

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76. A method of detecting expression of a taste receptor gene comprising (a) hybridizing at least one sample with a nucleic acid molecule according to Claim 1, and (b) detecting expression of the taste receptor gene by a positive hybridization signal.

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77. A method of screening a library comprising (a) hybridizing the library with a nucleic acid molecule according Claim 1 and (b) detecting one or more taste receptor clones in the library by a positive hybridization signal.

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78. A recombinant polynucleotide comprising a nucleic acid molecule according to Claim 1 which is attached directly or indirectly to a heterologous nucleic acid molecule.

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79. An expression vector comprising a nucleic acid molecule according to Claim 1, wherein the nucleic acid molecule is operably linked to a heterologous nucleic acid molecule that drives expression thereof.

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80. A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

81. A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

82. A method of making a recombinant polynucleotide comprising ligating a nucleic acid molecule according to Claim 1 to a heterologous nucleic acid.

5 83. The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

84. A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 78 into a host cell, or propagating the host cell
10 in which the recombinant polynucleotide has been introduced.

85. A method of detecting specific binding of a putative ligand to a taste receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the taste receptor is
15 expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the taste receptor.

86. A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-
20 human organism, or propagating the host non-human organism in which the recombinant polynucleotide has been introduced.

87. An isolated polypeptide molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from
25 the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24.

88. The isolated polypeptide molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

30 89. The isolated polypeptide molecule of Claim 87, wherein the fragment contains at least 150 amino acids.

90. The isolated polypeptide molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

91. The isolated polypeptide molecule of Claim 87, wherein the fragment
5 contains at least 250 amino acids.

92. The isolated polypeptide molecule of Claim 87, wherein the fragment is a T2R polypeptide.

10 93. The isolated polypeptide molecule of Claim 87, wherein the fragment specifically binds a tastant associated with a bitter substance selected from the group consisting of 6-n-propylthiouracil, sucrose octaacetate, raffinose undecaacetate, cycloheximide, denatonium, copper glycinate, and quinine.

15 94. A recombinant polypeptide comprising the polypeptide of Claim 87 and a heterologous peptide domain.

95. The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a transmembrane region of a G Protein-Coupled Receptor.
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96. The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with a taste receptor ligand-binding region, wherein the taste receptor ligand-binding region is a chimera of at least two different taste receptors.

25 97. A method of detecting specific binding of a ligand to a taste receptor comprising (a) contacting the ligand with the polypeptide of Claim 87, and (b) directly or indirectly detecting specific binding between the ligand and the taste receptor.

98. An antibody or antibody fragment that specifically binds a polypeptide
30 having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24.

99. A method of detecting specific binding of the antibody of Claim 98 to a taste receptor comprising (a) contacting the antibody with a sample which may contain the taste receptor and (b) detecting specific binding therebetween.

5 100. The method of Claim 99, wherein specific binding of the antibody to a cell in the sample identifies the cell as a taste cell.

101. A method of screening a library of chemical compounds for compounds that are involved in taste sensation comprising contacting compounds in
10 said library with at least one polypeptide according to Claim 87 and identifying compounds that specifically bind to at least one of said polypeptides.

102. The method of Claim 101 wherein said library is a combinatorial chemical library.

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103. The method of Claim 101 wherein said library is a peptide library.

104. The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal
20 peptidomimetic, or small molecule organic compound library.

105. The method of Claim 101 wherein said library is a random combination of compounds.

25 106. The method of Claim 101 wherein said compounds are screened by high throughput screening.

107. The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.
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108. A cell or non-human animal assay for identifying molecules that interact with a T2R polypeptide comprising:

obtaining a cell or non-human animal that expresses at least one functional T2R polypeptide or a chimeric polypeptide comprising a functional T2R polypeptide, and which optionally expresses at least one functional G Protein;

contacting said cell or non-human animal with a molecule to be screened for
5 its ability to modulate a T2R polypeptide; and
detecting whether modulation occurs.

109. The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.
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110. The method of Claim 108 wherein modulation is detected by measuring the transfer of ³²P from gamma-labeled GTP to the T2R polypeptide.

111. The method of Claim 108 wherein modulation is determined based on
15 a comparison to a control compound known to modulate the particular T2R polypeptide.

112. The method of Claim 108 wherein the G Protein is Gα15 or Gα16 or another promiscuous G Protein.
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113. The method of Claim 108 wherein modulation is determined by detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114. The method of Claim 108 wherein modulation is determined based on
25 the level of transcription a predetermined target protein after contacting the cell with the screened compound.

115. The method of Claim 108 when said screened compounds are synthesized by computer assisted compound design based on the predicted or actual
30 three-dimensional structure of the amino acid sequence of the T2R polypeptide or a fragment thereof.

116. The method of Claim 108 wherein compounds that modulate T2R polypeptides are identified based on whether they specifically bind to a T2R polypeptide.

5 117. The method of Claim 108 wherein modulation refers to the inhibition of T2R polypeptide function.

118. The method of Claim 108 wherein modulation refers to the enhancement of T2R polypeptide function.

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119. A method for representing the perception of one or more tastes in one or more mammals, comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n taste receptors of said mammals; and

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generating from said values a quantitative representation of taste perception, wherein at least one of said taste receptors is a taste receptor polypeptide having a sequence that is at least about 75% identical to a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24.

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120. The method of claim 119, wherein said representation constitutes a point or a volume in n -dimensional space.

121. The method of claim 119, wherein said representation constitutes a graph or a spectrum.

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122. The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

123. The method of claim 119, wherein said providing step comprises
30 contacting a plurality of recombinantly produced taste receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

124. A method for predicting the taste perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each
5 of n taste receptors of said mammal, for one or more molecules or combinations of molecules yielding known taste perception in a mammal,

generating from said values a quantitative representation of taste perception in a mammal for the one or more molecules or combinations of molecules yielding known taste perception in a mammal;

10 providing values X_1 to X_n representative of the quantitative stimulation of each of n taste receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown taste perception in a mammal;

generating from said values a quantitative representation of taste perception in a mammal for the one or more molecules or combinations of molecules yielding
15 unknown taste perception in a mammal; and

predicting the taste perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown taste perception in a mammal by comparing the quantitative representation of taste perception in a mammal generated by one or more molecules or combinations of molecules yielding
20 unknown taste perception in a mammal to the quantitative representation of taste perception in a mammal for the one or more molecules or combinations of molecules yielding known taste perception in a mammal,

wherein at least one of said taste receptors is a taste receptor polypeptide having a sequence that is at least about 75% identical to a sequence selected from the
25 group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, and 24.

125. An isolated nucleic acid molecule which exhibits at least 20-30% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 22, or which exhibits at least 30% sequence identity to a
30 fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence; and which further contains at least one sequence that encodes a polypeptide

which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

126. An isolated nucleic acid molecule which exhibits at least 40-60% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 22, or which exhibits at least 40-60% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

127. An isolated nucleic acid molecule that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 22, or at least 70% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof and; which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

128. An isolated nucleic acid molecule that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 22, or at least 90% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

129. An isolated nucleic acid molecule that exhibits at least 85% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 21 and 22, or at least 85% sequence identity with a fragment thereof comprising at least 100 contiguous nucleotides thereof; and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus

sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

130. An isolated nucleic acid molecule that exhibits at least 90% sequence
5 identity with a nucleic acid sequence selected from the group consisting of SEQ ID
NOS: 21 and 22, or at least 90% sequence identity with a fragment thereof comprising
at least 100 contiguous nucleotides thereof; and which further contains at least one
sequence that encodes a polypeptide which is at least 70% identical to a consensus
sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and
10 30.

131. An isolated nucleic acid molecule that exhibits at least 95% sequence
identity with a nucleic acid sequence selected from the group consisting of SEQ ID
NOS: 21 and 22, or at least 95% sequence identity with a fragment thereof comprising
15 at least 100 contiguous nucleotides thereof; and which further contains at least one
sequence that encodes a polypeptide which is at least 70% identical to a consensus
sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and
30.

132. An isolated nucleic acid molecule that exhibits about 95-99% sequence
20 identity with a nucleic acid sequence selected from the group consisting of SEQ ID
NOS: 21 and 22, or about 95-99% sequence identity with a fragment thereof
comprising at least 100 contiguous nucleotides thereof; and which further contains at
least one sequence that encodes a polypeptide which is at least 70% identical to a
25 consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27,
28, 29, and 30.

133. An isolated nucleic acid molecule having a nucleic acid sequence
selected from the group consisting of SEQ ID NOS: 21 and 22, or a fragment thereof
30 comprising at least 100 contiguous nucleotides thereof; and which further contains at
least one sequence that encodes a polypeptide which is at least 70% identical to a

consensus sequence selected from the group consisting of SEQ ID NOS: 25, 26, 27, 28, 29, and 30.

134. A method of screening a library comprising (a) hybridizing the library
5 with an isolated nucleic acid molecule according to Claim 125 and (b) detecting one or more taste receptor clones in the library by a positive hybridization signal.

135. A method of detecting expression of a G Protein-Coupled Receptor polypeptide gene in a cell comprising:
10 contacting said cell with a nucleic acid molecule that hybridizes to an isolated nucleic acid molecule according to claim 125 under stringent conditions; and
detecting hybridization in order to detect expression of said G Protein-Coupled Receptor polypeptide gene.

136. A method for screening a mammalian genome for a coding sequence for a G Protein-Coupled Receptor polypeptide active in taste signaling, comprising:

(i) contacting said mammalian genome with at least one degenerate primer consisting essentially of a nucleic acid sequence encoding a consensus sequence of SEQ ID NOS: 25, 26, 27, 28, 29, and 30, or at least one degenerate primer derived
20 from an isolated nucleic acid molecule according to claim 125;

(ii) amplifying said genomic sequence comprising said at least one primer sequence in the presence of polymerase, free nucleotides and cofactors; and

(iii) detecting the presence of an amplified sequence comprising a G Protein-Coupled Receptor polypeptide gene.

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137. A biochemical assay for identifying tastant ligands having binding specificity for a G Protein-Coupled Receptor active in taste signaling, comprising:

(i) contacting one or more polypeptides according to claim 87 with a preparation of G Proteins and GTP γ S, and one or more putative tastant ligands or a
30 composition comprising one or more putative tastant ligands; and

(ii) detecting binding of a tastant ligand having binding specificity for said G Protein-Coupled Receptor active in taste signaling by measuring the binding of GTP γ S to the G Protein.